Amendments to the Claims

Please amend claims 6, 16, 23 and 26; and add new claims 31-40 as presented below in the listing of claims. Please cancel claims 8-15, 17-22, 24, 25 and 27-30 without prejudice. This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of claims:

1. (original) A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and

b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

2. (original) A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;

b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and

c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

3. (original) A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;

b) choosing a variant selected from the group consisting of:

i) a variant which comprises preferred primary anchor residues of said motif; and

ii) a variant which occurs with high frequency within the population of variants; and

c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

4. (original) A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising

a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;

b) choosing a variant selected from the group consisting of:

i) a variant which comprises preferred primary anchor residues of said motif; and

ii) a variant which occurs with high frequency within the population of variants; and

c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and

d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

5. (original) The method of claim 1, wherein (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

6. (currently amended) The method of claim 2 ~~or 3~~, wherein (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

7. (original) The method of claim 4, wherein (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

8-15. (canceled)

16. (currently amended) The method of claim 1 ~~any of claims 1-15~~, wherein the infectious agent is selected from the group consisting of : HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, [[and]] Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis, Chlamydia, Candida albicans, Cryptococcus neoformans, Coccidoides spp., Histoplasma spp, Aspergillus fumigatis, Plasmodium spp., Trypanosoma spp., Schistosoma spp.*, and [[*and*]] *Leishmania spp.*

17-22. (canceled)

23. (currently amended) The method of claim 1 ~~any claims 1-4~~, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.

24-25. (canceled)

26. (currently amended) The method of claim 1 ~~any of claims 1-4~~, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.

27-30. (canceled)

31. (new) The method of claim 3, wherein (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

32. (new) The method of claim 2, wherein the infectious agent is selected from the group consisting of : HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis, Chlamydia, Candida albicans, Cryptococcus neoformans, Coccidoides spp., Histoplasma spp,*

Aspergillus fumigatis, Plasmodium spp., Trypanosoma spp., Schistosoma spp., and *Leishmania spp.*

33. (new) The method of claim 3, wherein the infectious agent is selected from the group consisting of : HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis, Chlamydia, Candida albicans, Cryptococcus neoformans, Coccidoides spp., Histoplasma spp, Aspergillus fumigatis, Plasmodium spp., Trypanosoma spp., Schistosoma spp.*, and *Leishmania spp.*

34. (new) The method of claim 4, wherein the infectious agent is selected from the group consisting of : HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis, Chlamydia, Candida albicans, Cryptococcus neoformans, Coccidoides spp., Histoplasma spp, Aspergillus fumigatis, Plasmodium spp., Trypanosoma spp., Schistosoma spp.*, and *Leishmania spp.*

35. (new) The method of claim 2, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.

36. (new) The method of claim 3, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.

37. (new) The method of claim 4, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.

38. (new) The method of claim 2, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.

39. (new) The method of claim 3, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.

40. (new) The method of claim 4, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.